

A:Molecule type: protein
A:Residues: 228-241:265-272:458-464:467-488 <MO2>
C:Genetics:
A:Map position: 4COP9-4G3845
C:Function:

A:Description: hydrolyzes 1,4-glycosidic linkages of starch, removing maltose units suc
C:Superfamily: beta-amylase
C:Keywords: glycosidase; hydrolase; monomer; polysaccharide degradation
F:2-499/Product: beta-amylase #status predicted <MAY>
F:190,384/Active site: Glu #status predicted

Query Match 35.1%; Score 1092.5; DB 1; Length 499;
Best Local Similarity 47.5%; Pred. No. 6.9e-78;
Matches 210; Conservative 84; Mismatches 137; Indels 11; Gaps 8;

QY 112 VPVFMPLDSVKMDHTVNRKKAMNASLOALK-SAGVEGIMDMVWGLVERDAPGEYNWG 170
DB 14 VPVFMPLDSVKMDHTVNRKKAMNASLOALK-SAGVEGIMDMVWGLVERDAPGEYNWG 170
QY 171 GYAELEMAKHHGLKVAQVMSFHQCGNGVDSCTIPLPRVWVEEMKDPDLAYTDQWGR 230
DB 74 AYKTLFOLIARGLKIAQIMSFHQCGNGVDSCTIPLPRVWVEEMKDPDLAYTDQWGR 230
QY 231 NFEVSLGCDTLPVLKGTPTVQCYSDFMGRFRDENLL-GDTIVEIQVGMGPAGELRY 288
DB 134 DIEVLSIGVDNLPFLAGRTAVQVLYSDYMSFKNMADLIEAGVIVDIEVGLGPAGELRY 193
QY 289 PSYPEKGVKFKFCIGAFQCYDKYMISSLOGAAAEAFKPEWCHTGPDPAGQYNNPDTN 348
DB 194 PSYQSGQ-WFFPGIGFQCYDKYKDFKAAKAGHPDWL--PEDAGEYNDKPEETG 250
QY 349 FFKKEGGWDSOYGEFFLTWYSEMLNHRGILQSAKAIFEKGVKISVKIAGIHHYGT 408
DB 251 FFKKD-GTYVSEKGFPTWYNNKLIIFHQDILGEANKIFAGLVNLAAGVGIHLYNH 309
QY 409 RSHAPETAGYNNTRNDGYLPIAQMUAHGAVFNFCTVEMRDHEQPDALCAPEKLVYRQ 468
DB 310 HSHAAELTAGYNNLFKRDGYRPIARMSKHGILNFCTLEMKDNTDAEALSAPQELVQE 369
QY 469 VALATQEAQVPLAGENALPRYDDYAHQIIL--OASSLNINDQSGDREMCFAFTYLRNPD 525
DB 370 VLSKAWKEGIEVAGNALETYGAQYNNQIILNARPNVNGPKKLR-MYGFITYLRUSD 428
QY 526 LFHPDNRFRFAFKMKKEGKD 547
DB 429 VFQENNELFKLVKMKHAQDQ 450

RESULT 13
C84731
probable beta-amylase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: C84731
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: C84731
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-505 <STO>
A:Cross-references: GB:AE002093; NID:g3831467; PIDN:AAC69949.1; GSPDB:GN00139
C:Genetics:
A:Map position: 2
C:Superfamily: beta-amylase

Query Match 35.1%; Score 1092.5; DB 2; Length 505;
Best Local Similarity 44.4%; Pred. No. 7e-78;
Matches 204; Conservative 89; Mismatches 155; Indels 11; Gaps 4;

QY 112 VPVFMPLDSVKMDHTVNRKKAMNASLOALK-SAGVEGIMDMVWGLVERDAPGEYNWG 171
DB 6 VPVFMPLDSVKMDHTVNRKKAMNASLOALK-SAGVEGIMDMVWGLVERDAPGEYNWG 171
QY 172 YAELEMAKHHGLKVAQVMSFHQCGNGVDSCTIPLPRVWVEEMKDPDLAYTDQWGR 231
DB 66 YRNLFAIVQSFGKLAQIMSFHQCGNGVDSCTIPLPRVWVEEMKDPDLAYTDQWGR 231
QY 232 FEVSLGCDTLPVLKGTPTVQCYSDFMGRFRDENLLGD-TIVEIQVGMGPAGELRYPS 290
DB 126 KECLSLVDNLSLFRGTAVEMRYDMKSFRENEDFISSGVIIDIEVGLGPAGELRYPS 185
QY 291 YPKDGVKWKFGIGAFQCYDKYMISSLOGAAAEAFKPEWCHTGPDPAGQYNNPDTN 350
DB 186 YSETQG-WFFPGIGFQCYDKYLSYEEVRRIGHPEW--KLPENAGEVNSYGETEFT 242
QY 351 KKEGGWDSOYGEFFLTWYSEMLNHRGILQSAKAIFEKGVKISVKIAGIHHYGT 410
DB 243 EYNGTYLKEEGNFFLSWYSKLLHGDQILDANKVFLGCKLKAIAKVSIGIHWYKTES 302
QY 411 HAPETAGYNNTRNDGYLPIAQMUAHGAVFNFCTVEMRDHEQPDALCAPEKLVYRQ 470
DB 303 HAAELTAGYNNLRDGYRAIKMRHRAILNFTCLEMKNTEQPAKAKSGPOELVQVQL 362
QY 471 LATQEAQVPLAGENALPRYDDYAHQIILQASSLNINDQSGDREMCFAFTYLRNPD 530
DB 363 SSGWRGIEVAGENALPRDRNGYNNQIILNARPNVNGQDKPRMFGFTYLRSLDKLLNEP 422
QY 531 NWRFRFAFKMKKEGKDANKREQVEREAHFVHIITQPL 569
DB 423 NFSTFKMFLKRM-----HANQCYCEPERYNHLLPL 454

RESULT 14
JQ2248
beta-amylase (EC 3.2.1.2) - rye
N:Alternate names: 1,4-alpha-D-glucan maltohydrolase
C:Species: Secale cereale (rye)
C:Date: 03-May-1994 #sequence_revision 25-Oct-1996 #text_change 28-May-1999
C:Accession: JQ2248
R:Sadowski, J.; Korat, T.; Cooke, R.; Delseny, M.
Plant Physiol. 102, 315-316, 1993
A:title: Nucleotide sequence of a cDNA clone encoding ubiquitous beta-amylase in rye
A:Reference number: JQ2248; MUID:94151427; PMID:8108499
A:Accession: JQ2248
A:Molecule type: mRNA
A:Residues: 1-503 <SAD>
A:Cross-references: GB:Z11772; NID:g393449; PIDN:CAA77817.1; PID:g393450
C:Function:

A:Description: hydrolyzes 1,4-glycosidic linkages of starch, removing maltose units s
C:Superfamily: beta-amylase
C:Keywords: glycoprotein; glycosidase; hydrolase; monomer; polysaccharide degradation
F:2-503/Product: beta-amylase #status predicted <MAY>
F:184,378/Active site: Glu #status predicted
F:249,338/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 34.6%; Score 1079.5; DB 1; Length 503;
Best Local Similarity 48.6%; Pred. No. 7.3e-77;
Matches 211; Conservative 74; Mismatches 142; Indels 7; Gaps 6;

QY 112 VPVFMPLDSVKMDHTVNRKKAMNASLOALK-SAGVEGIMDMVWGLVERDAPGEYNWG 171
DB 10 VQVFMPLDSVKMDHTVNRKKAMNASLOALK-SAGVEGIMDMVWGLVERDAPGEYNWG 171
QY 172 YAELEMAKHHGLKVAQVMSFHQCGNGVDSCTIPLPRVWVEEMKDPDLAYTDQWGR 231
DB 70 YKQVFDLVHAGLKLQAIMSFHQCGNGVDSCTIPLPRVWVEEMKDPDLAYTDQWGR 231
QY 232 FEVSLGCDTLPVLKGTPTVQCYSDFMGRFRDENLL-GDTIVEIQVGMGPAGELRYPS 290
DB 130 IEYTLGVDQDPLFHGRTAVQYADYNASFRNKKRFLDAGTIVDIEVGLGPAGELRYPS 189